



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 153618

TO: Nita M Minnifield  
Location: rem/3c01/3c18  
Art Unit: 1645  
Wednesday, May 18, 2005

Case Serial Number: 09/942098

From: Mary Jane Ruhl  
Location: Biotech-Chem Library  
Remsen 1-A-62  
Phone: 571-272-2524

maryjane.ruhl@uspto.gov

### Search Notes

Examiner Minnifield,

Here are the results for your recent search request.

Please feel free to contact me if you have any questions about these results.

Thank you for using STIC services. We appreciate the opportunity to serve you.

Sincerely,

Mary Jane Ruhl  
Technical Information Specialist  
STIC  
Remsen 1-A-62  
Ext. 22524

*Reviewed  
5/30/05  
mr*



STIC-Biotech/ChemLib

153 618

Mg

From: Chan, Christina  
Sent: Tuesday, May 17, 2005 8:55 AM  
To: Minnifield, Nita; STIC-Biotech/ChemLib  
Subject: RE: interference sequence search

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
(571)-272-0841  
Remsen, 3E89

RECEIVED  
MAY 17 2005  
15:16

-----Original Message-----

From: Minnifield, Nita  
Sent: Monday, May 16, 2005 6:51 PM  
To: Chan, Christina  
Subject: interference sequence search

Christina,  
Please approve, 2 month amdt. due.

STIC 09/942098

Please do a commercial and interference sequence search on SEQ ID NO: 30 of this application.

Please do an interference sequence search on SEQ ID NO: 1 and 2, and aa 187-203 of SEQ ID NO: 2.

Please provide a paper copy of all results.

Thanks,  
Minnifield,  
71976  
Art Unit 1645  
Office REM-3C01  
Mailbox REM-3C18  
571-272-0860

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: \_\_\_\_\_ AA#: \_\_\_\_\_  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 17, 2005, 15:24:21 ; Search time 175 Seconds  
(without alignments)  
49.745 Million cell updates/sec

Title: US-09-942-098-30

Perfect score: 83

Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	124	2	Q93578 brachydanio
2	83	100.0	143	2	Q9GM34 macaca fasc
3	83	100.0	198	2	Q6PC84 brachydanio
4	83	100.0	203	1	SN2B_CARAU
5	83	100.0	203	2	Q93579 carassius a
6	83	100.0	203	2	Q6PC54 brachydanio
7	83	100.0	204	1	SN2A_CARAU
8	83	100.0	204	2	Q705J6 carassius a
9	83	100.0	206	1	SN25_CHICK
10	83	100.0	206	1	SN25_HUMAN
11	83	100.0	206	1	SN25_MACMU
12	83	100.0	206	1	SN25_MOUSE
13	83	100.0	206	1	SN25_RAT
14	79	95.2	204	2	Q6P3L7 brachydanio
15	69	83.1	206	2	Q8AXM1 xenopus lae
16	69	83.1	206	2	Q8AXM2 xenopus lae
17	69	83.1	206	2	Q640W4 xenopus lae
18	66	79.5	214	2	Q7ZVE4 brachydanio
19	65	78.3	210	1	SN25_TORMA
20	65	78.3	212	2	Q8T3S4 loligo peal
21	61	73.5	137	2	Q66ID7 brachydanio
22	60	72.3	204	2	Q8JIS7 xenopus lae
23	53	63.9	212	2	O01389 hiruodo medi
24	50	60.2	210	1	SN23_MOUSE
25	50	60.2	210	1	SN23_RAT
26	50	60.2	221	1	Q9D3L3 mus musculus
27	47	56.6	220	2	Q859G6 lymnaea sca
28	46	55.4	211	1	SN23_HUMAN
29	46	55.4	2315	2	Q952K3 caenorhabdi
30	46	55.4	2350	2	Q7JNN3 caenorhabdi
31	46	55.4	2396	2	Q23081 caenorhabdi

32	45	54.2	83	2	O85431 pseudomonas
33	45	54.2	83	2	O85439 pseudomonas
34	45	54.2	83	2	O85440 pseudomonas
35	45	54.2	125	2	O96576 leucophaea
36	45	54.2	212	1	SN25_DROME
37	44.5	53.6	191	2	Q8ZV72 drosophila
38	44	53.0	90	2	O96578 leucophaea
39	44	53.0	207	2	O62414 caenorhabdi
40	44	53.0	213	2	Q7PUS1 anopheles g
41	44	53.0	649	2	Q7NAR4 mycoplasma
42	44	53.0	776	2	Q89Q18 bradyrhizob
43	43.5	52.4	2090	1	NIN HUMAN
44	43.5	52.4	55	2	Q8NCR8 homo sapien
45	43	51.8	353	2	Q8FNU8 corynebacte

ALIGNMENTS

RESULT 1  
O93578 PRELIMINARY; PRT; 124 AA.  
AC O93578;  
DT 01-NOV-1998 (TREMREL. 08, Created)  
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)  
DE 01-MAR-2004 (TREMREL. 26, Last annotation update)  
DE Synaptoosome-associated protein 25.1 (Fragment).  
GN Name-snap25a; Synonyms=Snap;  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99057281; PubMed=9843147;  
RX DOI=10.1007/(SICI)1097-4547(19981201)54:5<563::AID-JNRI>3.3.CO;2-Z;  
RA Risinger C., Salaneck E., Soderberg C., Gates M., Postlethwait J.H.,  
RA Larhammar D.,  
RT "Cloning of two loci for synapse protein Snap25 in zebrafish:  
RT comparison of paralogous linkage groups suggests loss of one locus in  
RT the mammalian lineage."  
RL J. Neurosci. Res. 54:563-573(1998).  
CC -!- SIMILARITY: Belongs to the SNAP-25 family.  
DR EMBL; AF091593; AAC64289.1; -.  
DR HSSP; Q8T384; IL4A.  
DR ZFIN; ZDB-GENE-980526-468; snap25a.  
DR GO; GO:0019717; C:synaptoosome; IEA.  
DR GO; GO:0003700; P:transcription factor activity; IEA.  
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.  
DR InterPro; IPR002197; HTH\_F18.  
DR InterPro; IPR000928; SNAP-25.  
DR InterPro; IPR010989; t-snare.  
DR InterPro; IPR000727; T-SNARE.  
DR Pfam; PF00835; SNAP-25; 1.  
DR Pfam; PF05739; SNARE; 1.  
DR PRINTS; PR01590; HTHFIS.  
DR SMART; SM00397; t-SNARE; 1.  
DR PROSITE; PS50192; T-SNARE; 1.  
FT NON\_TER  
SQ SEQUENCE 124 AA; 13616 MW; 50E27DBDB33D958C CRC64;

Query Match 100.0%; Score 83; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 3.2e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SNKTRIDEANQRATKML 17  
DB 105 SNKTRIDEANQRATKML 121

RESULT 2

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OM protein - protein search, using sw model

Run on: May 17, 2005, 15:25:17 ; Search time 38 Seconds  
(without alignments)  
43.044 Million cell updates/sec

Title: US-09-942-098-30  
Perfect score: 83  
Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	203	2 I50481	synapse protein SN
2	83	100.0	204	2 I50480	synapse protein SN
3	83	100.0	206	2 A37861	synaptosomal-assoc
4	83	100.0	206	2 I53735	nerve terminal pro
5	83	100.0	206	2 I67823	synaptosomal-assoc
6	83	100.0	206	2 A33623	synapse protein 23 -
7	65	78.3	210	2 I50552	SNARE protein 23 -
8	50	60.2	210	2 I50512	vesicle-membrane f
9	46	55.4	158	2 JCS297	vesicle-membrane f
10	46	55.4	211	2 JCS296	hypothetical prote
11	46	55.4	2288	2 T29999	hypothetical prote
12	44	53.0	234	2 T26553	outer membrane lip
13	42	50.6	83	2 A33854	transmembrane tran
14	42	50.6	401	2 E81436	hypothetical prote
15	42	50.6	420	2 S50562	hypothetical prote
16	41	49.4	393	2 T32127	hypothetical prote
17	41	49.4	494	2 S64386	pre-mRNA splicing
18	41	49.4	642	2 G90551	lipoprotein (impor
19	40	48.2	540	2 T31487	hypothetical prote
20	40	48.2	575	2 F96966	methyl-accepting c
21	39.5	47.6	1314	2 T03481	matng type silenc
22	39	47.0	243	2 T20653	hypothetical prote
23	39	47.0	680	2 H70347	outer membrane pro
24	38.5	46.4	918	2 G88545	protein F59B2.12 l
25	38.5	46.4	943	2 S31132	hypothetical prote
26	38	45.8	142	2 T48816	hypothetical prote
27	38	45.8	151	2 G95369	SyrB2 transcriptio
28	38	45.8	176	2 D72668	hypothetical prote
29	38	45.8	181	2 A45422	ADP-ribosylation f

30 38 45.8 181 2 JC4946 ADP-ribosylation f  
31 38 45.8 217 2 A47483 cysteine-rich omeg  
32 38 45.8 219 2 AB1996 hypothetical prote  
33 38 45.8 294 2 S68784 cathepsin L - Para  
34 38 45.8 317 2 A72295 conserved hypochet  
35 38 45.8 414 2 T26205 hypothetical prote  
36 38 45.8 465 2 T16618 hypothetical prote  
37 38 45.8 586 1 C64988 probable sulfatase  
38 38 45.8 586 2 H91013 probable sulfatase  
39 38 45.8 586 2 H85858 probable sulfatase  
40 38 45.8 643 2 T32269 hypothetical prote  
41 38 45.8 869 2 H89864 hypothetical prote  
42 38 45.8 1272 2 C96637 hypothetical prote  
43 38 45.8 1578 2 S76238 hypothetical prote  
44 37 44.6 150 2 T19447 hypothetical prote  
45 37 44.6 227 2 D83271 probable ATP-bind

ALIGNMENTS

RESULT 1

I50481  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50481  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A>Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50481  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-203 <RIS>  
A:Cross-references: UNIPROT:P36978; GB:L22976; NID:G349430; PIDN:AAA16538.1; PID:G34943  
C:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 83; DB 2; Length 203;  
Best Local Similarity 100.0%; Pred. No. 8.6e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17  
DB 184 SNKTRIDEANQRATKML 200  
|||||

RESULT 2

I50480  
synapse protein SNAP-25 - goldfish  
C:Species: Carassius auratus (goldfish)  
C>Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C:Accession: I50480  
R:Risinger, C.; Larhammar, D.  
Proc. Natl. Acad. Sci. U.S.A. 90, 10598-10602, 1993  
A>Title: Multiple loci for synapse protein SNAP-25 in the tetraploid goldfish.  
A:Reference number: A49632; MUID:94068448; PMID:8248151  
A:Accession: I50480  
A>Status: preliminary; translated from GB/EMBL/DBDJ  
A:Molecule type: mRNA  
A:Residues: 1-204 <RIS>  
A:Cross-references: UNIPROT:P36977; GB:L22973; NID:G349426; PIDN:AAA16537.1; PID:G34942  
C:Genetics:  
A:Gene: SNAP-25

Query Match 100.0%; Score 83; DB 2; Length 204;  
Best Local Similarity 100.0%; Pred. No. 8.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17  
DB 185 SNKTRIDEANQRATKML 201  
|||||

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OM protein - protein search, using sw model

Run on: May 17, 2005, 15:26:17 ; Search time 44 Seconds  
(without alignments)  
28.842 Million cell updates/sec

Title: US-09-942-098-30

Perfect score: 83

Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/prodata/1/iaa/5A COMB.pdp.\*

2: /cgn2\_6/prodata/1/iaa/5B COMB.pdp.\*

3: /cgn2\_6/prodata/1/iaa/6A COMB.pdp.\*

4: /cgn2\_6/prodata/1/iaa/6B COMB.pdp.\*

5: /cgn2\_6/prodata/1/iaa/PCUTUS COMB.pdp.\*

6: /cgn2\_6/prodata/1/iaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	2	US-08-743-894B-1
2	83	100.0	17	2	US-08-743-894B-37
3	83	100.0	20	3	US-08-819-286-9
4	83	100.0	26	3	US-08-819-286-8
5	83	100.0	37	3	US-08-819-286-4
6	83	100.0	70	2	US-08-760-001-10
7	83	100.0	70	3	US-09-015-960-10
8	83	100.0	70	3	US-09-534-572-10
9	83	100.0	116	4	US-09-962-360B-11
10	83	100.0	206	1	US-08-393-985-18
11	83	100.0	206	3	US-08-819-286-1
12	83	100.0	206	4	US-09-949-016-6311
13	83	100.0	219	4	US-09-949-016-10671
14	80	96.4	17	2	US-08-743-894B-18
15	80	96.4	17	2	US-08-743-894B-43
16	79	95.2	16	2	US-08-743-894B-49
17	79	95.2	17	2	US-08-743-894B-27
18	79	95.2	17	2	US-08-743-894B-30
19	79	95.2	17	2	US-08-743-894B-32
20	79	95.2	17	2	US-08-743-894B-39
21	78	94.0	17	2	US-08-743-894B-19
22	78	94.0	17	2	US-08-743-894B-25
23	78	94.0	17	2	US-08-743-894B-29
24	78	94.0	17	2	US-08-743-894B-42
25	78	94.0	17	2	US-08-743-894B-50
26	77	92.8	17	2	US-08-743-894B-2
27	77	92.8	17	2	US-08-743-894B-20

28	77	92.8	17	2	US-08-743-894B-24	Sequence 24, Appl
29	77	92.8	17	2	US-08-743-894B-26	Sequence 26, Appl
30	77	92.8	17	2	US-08-743-894B-28	Sequence 28, Appl
31	77	92.8	17	2	US-08-743-894B-31	Sequence 31, Appl
32	77	92.8	17	2	US-08-743-894B-33	Sequence 33, Appl
33	77	92.8	17	2	US-08-743-894B-34	Sequence 34, Appl
34	77	92.8	17	2	US-08-743-894B-36	Sequence 36, Appl
35	77	92.8	17	2	US-08-743-894B-44	Sequence 44, Appl
36	77	92.8	17	2	US-08-743-894B-46	Sequence 46, Appl
37	77	92.8	17	2	US-08-743-894B-48	Sequence 48, Appl
38	77	92.8	17	2	US-09-962-360B-8	Sequence 8, Appl
39	77	92.8	116	4	US-09-962-360B-12	Sequence 12, Appl
40	75	90.4	17	2	US-08-743-894B-21	Sequence 21, Appl
41	75	90.4	17	2	US-08-743-894B-35	Sequence 35, Appl
42	75	90.4	17	2	US-08-743-894B-47	Sequence 47, Appl
43	75	90.4	17	2	US-08-743-894B-48	Sequence 48, Appl
44	74	89.2	15	2	US-08-743-894B-38	Sequence 38, Appl
45	74	89.2	17	2	US-08-743-894B-3	Sequence 3, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-743-894B-1

; Sequence 1, Application US/08743894B

; Patent No. 5965699

; GENERAL INFORMATION:

; APPLICANT: James J. Schmidt

; APPLICANT: Karen A. Bostian

; TITLE OF INVENTION: Assay for the Proteolytic Activity of Serotype A Neurotoxin F

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MCMC-JA Attn:John Moran-Patent Atty

; STREET: USA MCMC - 504 Scott Street

; CITY: FORT DETRICK

; STATE: MARYLAND

; COUNTRY: USA

; ZIP: 21702-5012

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 7.0

; SOFTWARE: Microsoft Word 6.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/743,894B

; FILING DATE: No. 5965699ember 6, 1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Charles H. Harris

; REGISTRATION NUMBER: 34,616

; REFERENCE/DOCKET NUMBER:

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 619-2065

; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 17 amino acids

; TYPE: amino acid sequence

; STRANDEDNESS: Single

; TOPOLOGY: Linear

US-08-743-894B-1

Query Match

Best Local Similarity 100.0%; Score 83; DB 2; Length 17;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY

1 SNKTRIDEANORATKML 17

DB

1 SNKTRIDEANORATKML 17

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OM protein - protein search, using sw model

Run on: May 17, 2005, 15:34:49 ; Search time 134 Seconds  
(without alignments)  
42.380 Million cell updates/sec

Title: US-09-942-098-30

Perfect score: 83  
Sequence: 1 SNKTRIDEANQRATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pap:\*
  - 2: /cgn2\_6/ptodata/2/pubppaa/PCT\_NEW\_PUB.pap:\*
  - 3: /cgn2\_6/ptodata/2/pubppaa/US06\_NEW\_PUB.pap:\*
  - 4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pap:\*
  - 5: /cgn2\_6/ptodata/2/pubppaa/US07\_NEW\_PUB.pap:\*
  - 6: /cgn2\_6/ptodata/2/pubppaa/PCTUS\_PUBCOMB.pap:\*
  - 7: /cgn2\_6/ptodata/2/pubppaa/US08\_NEW\_PUB.pap:\*
  - 8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pap:\*
  - 9: /cgn2\_6/ptodata/2/pubppaa/US09A\_PUBCOMB.pap:\*
  - 10: /cgn2\_6/ptodata/2/pubppaa/US09B\_PUBCOMB.pap:\*
  - 11: /cgn2\_6/ptodata/2/pubppaa/US09C\_PUBCOMB.pap:\*
  - 12: /cgn2\_6/ptodata/2/pubppaa/US09D\_PUBCOMB.pap:\*
  - 13: /cgn2\_6/ptodata/2/pubppaa/US10A\_PUBCOMB.pap:\*
  - 14: /cgn2\_6/ptodata/2/pubppaa/US10B\_PUBCOMB.pap:\*
  - 15: /cgn2\_6/ptodata/2/pubppaa/US10C\_PUBCOMB.pap:\*
  - 16: /cgn2\_6/ptodata/2/pubppaa/US10D\_PUBCOMB.pap:\*
  - 17: /cgn2\_6/ptodata/2/pubppaa/US10E\_PUBCOMB.pap:\*
  - 18: /cgn2\_6/ptodata/2/pubppaa/US11\_NEW\_PUB.pap:\*
  - 19: /cgn2\_6/ptodata/2/pubppaa/US60\_NEW\_PUB.pap:\*
  - 20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	83	100.0	17	10	US-09-942-024-30
2	83	100.0	17	10	US-09-942-098-30
3	83	100.0	17	13	US-10-011-588-2
4	83	100.0	17	15	US-10-261-161-52
5	83	100.0	17	15	US-10-261-161-58
6	83	100.0	18	10	US-09-942-024-32
7	83	100.0	18	10	US-09-942-098-32
8	83	100.0	18	15	US-10-261-161-54
9	83	100.0	21	10	US-09-942-024-89
10	83	100.0	21	10	US-09-942-098-89
11	83	100.0	23	10	US-09-942-024-88
12	83	100.0	23	10	US-09-942-098-88
13	83	100.0	24	10	US-09-942-024-90

14	83	100.0	24	10	US-09-942-098-90
15	83	100.0	33	10	US-09-942-024-33
16	83	100.0	33	10	US-09-942-024-37
17	83	100.0	33	10	US-09-942-024-38
18	83	100.0	33	10	US-09-942-098-33
19	83	100.0	33	10	US-09-942-098-37
20	83	100.0	33	10	US-09-942-098-38
21	83	100.0	33	15	US-10-261-161-55
22	83	100.0	33	15	US-10-261-161-59
23	83	100.0	33	15	US-10-261-161-60
24	83	100.0	116	10	US-09-942-024-14
25	83	100.0	203	10	US-09-942-098-14
26	83	100.0	203	10	US-10-261-161-7
27	83	100.0	203	15	US-09-942-024-2
28	83	100.0	206	10	US-09-942-024-7
29	83	100.0	206	10	US-09-942-024-12
30	83	100.0	206	10	US-09-942-098-2
31	83	100.0	206	10	US-09-942-098-7
32	83	100.0	206	10	US-09-942-098-12
33	83	100.0	206	10	US-09-942-098-2
34	83	100.0	206	15	US-10-261-161-4
35	83	100.0	206	15	US-10-261-161-5
36	83	100.0	206	15	US-10-261-161-109
37	83	100.0	206	16	US-10-318-417-3
38	80	96.4	17	10	US-09-942-024-55
39	80	96.4	17	10	US-09-942-098-55
40	80	96.4	17	15	US-10-261-161-80
41	79	95.2	16	10	US-09-942-024-29
42	79	95.2	16	10	US-09-942-098-29
43	79	95.2	16	15	US-10-261-161-51
44	79	95.2	16	15	US-10-261-161-67
45	79	95.2	17	10	US-09-942-024-31

ALIGNMENTS

RESULT 1  
US-09-942-024-30  
; Sequence 30, Application US/09942024  
; Publication No. US20030143650A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.  
; APPLICANT: Fernandez-Salas, Ester  
; APPLICANT: Aoki, Kei Roger  
; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
; FILE REFERENCE: P-AR 4803  
; CURRENT APPLICATION NUMBER: US/09/942,024  
; CURRENT FILING DATE: 2001-08-28  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-942-024-30

Query Match 100.0%; Score 83; DB 10; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2.6e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SNKTRIDEANQRATKML 17  
DB 1 SNKTRIDEANQRATKML 17

RESULT 2  
US-09-942-098-30  
; Sequence 30, Application US/09942098  
; Publication No. US20030143651A1  
; GENERAL INFORMATION:  
; APPLICANT: Steward, Lance E.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 17, 2005, 15:23:26 ; Search time 163 Seconds  
(without alignments)  
40.337 Million cell updates/sec

Title: US-09-942-098-30  
Perfect score: 83  
Sequence: 1 SNKTRIDEANORATKML 17

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	83	100.0	17	2	AAY44057 Human SNA
2	83	100.0	17	2	AAY44021 Amino aci
3	83	100.0	17	5	ABG69065 Human pol
4	83	100.0	17	6	AAE36675 Human SNA
5	83	100.0	17	7	ABW01731 Human SNA
6	83	100.0	17	8	ADM97046 Botulinum
7	83	100.0	17	8	ADM97062 Botulinum
8	83	100.0	18	6	AAE36677 Human SNA
9	83	100.0	18	7	ABW01733 Human SNA
10	83	100.0	18	8	ADM97048 Botulinum
11	83	100.0	19	4	AAE36678 Human SNA
12	83	100.0	19	8	ADP13171 SNAP 25 p
13	83	100.0	20	2	AAW30100 Neurotran
14	83	100.0	20	7	ABW01798 FRET subs
15	83	100.0	21	6	AAE36734 FRET subs
16	83	100.0	21	7	ABW01790 FRET subs
17	83	100.0	23	6	AAE36733 FRET subs
18	83	100.0	23	7	ABW01789 FRET subs
19	83	100.0	24	6	AAE36735 FRET subs
20	83	100.0	24	7	ABW01791 FRET subs
21	83	100.0	26	2	AAW30099 Neurotran
22	83	100.0	33	6	AAE36682 Goldfish
23	83	100.0	33	6	AAE36683 Goldfish
24	83	100.0	33	6	AAE36678 SNAP-25 p
25	83	100.0	33	7	ABW01739 Goldfish

26	83	100.0	33	7	ABW01734 Mouse SNA
27	83	100.0	33	7	ABW01738 Goldfish
28	83	100.0	33	8	ADM97054 Botulinum
29	83	100.0	33	8	ADM97053 Botulinum
30	83	100.0	33	8	ADM97049 Botulinum
31	83	100.0	37	2	AAW30097 Neurotran
32	83	100.0	70	2	AAE36823 SNAP-25 p
33	83	100.0	86	4	AAE36823 SNAP-25 p
34	83	100.0	86	8	AAE36823 SNAP-25 p
35	83	100.0	116	5	AAO15165 Clostridi
36	83	100.0	200	8	ADN11044 Murine SN
37	83	100.0	203	7	ABW01715 Goldfish
38	83	100.0	203	8	ADM97001 Goldfish
39	83	100.0	206	2	AAW30103 Synapto
40	83	100.0	206	2	AAW30103 Synapto
41	83	100.0	206	2	AAW30103 Synapto
42	83	100.0	206	2	AAW30103 Synapto
43	83	100.0	206	4	AAU00253 SNARE hom
44	83	100.0	206	4	AAU00252 SNARE hom
45	83	100.0	206	6	AAE36662 Human SNA

ALIGNMENTS

RESULT 1

RAY44057	RAY44057 standard; peptide; 17 AA.
XX	AC
XX	AA44057;
XX	AC
DT	18-JAN-2000 (first entry)
XX	Human SNAP25 (amino acids 187-203) analogue #36.
DE	Human SNAP25 (amino acids 187-203) analogue #36.
KW	Enzymatic assay; quantitation; type A botulinum neurotoxin; proteolysis;
KW	fluorescamine; detection; human; synaptosomal protein; SNAP25;
KW	hydrolysis; amino group.
XX	Homo sapiens.
OS	Synthetic.
OS	Synthetic.
PN	US5965699-A.
XX	US5965699-A.
PD	12-OCT-1999.
XX	12-OCT-1999.
PF	06-NOV-1996; 96US-00743894.
XX	06-NOV-1996; 96US-00743894.
PR	06-NOV-1996; 96US-00743894.
XX	06-NOV-1996; 96US-00743894.
PA	(USSA ) US SEC OF ARMY.
XX	(USSA ) US SEC OF ARMY.
PI	Bostian KA, Schmidt JJ,
XX	Bostian KA, Schmidt JJ,
DR	WPI; 1999-579939/49.
XX	WPI; 1999-579939/49.
PT	Quantitation of type A botulinum toxin.
XX	Quantitation of type A botulinum toxin.
PS	Disclosure; Col 9; 28pp; English.
XX	Disclosure; Col 9; 28pp; English.
CC	The invention relates to an enzymatic assay for the quantitation of type
CC	A botulinum toxin, by determining the proteolytic activity of botulinum
CC	neurotoxin type A using fluorescamine detection. Botulinum toxin A has
CC	been shown to cleave the synaptosomal neurotransmitter peptide SNAP25
CC	between residues 197-198. The method comprises adding an analogue (e.g.
CC	human SNAP25) of the SNAP25 peptide (AAY44021, amino acids 187-203 of
CC	human SNAP25) to a sample containing the botulinum toxin A so that
CC	hydrolysis of the peptide is initiated, then stopping hydrolysis of the
CC	peptide at different time points; and measuring the amount of hydrolysis
CC	at each time point by combining with a label capable of detecting free
CC	amino groups resulting from the hydrolysis. The amount of botulinum toxin
CC	A present in the sample is determined by comparing measurements with the
CC	amount of label produced from a known concentration of toxin measured